```
GAP of: us-09-488-265-27  check: 2749  from: 1  to: 437

FROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/US0948265.pep
sequence 27, application us/09488265
general information:
applicant: lehmann, martin
applicant: lassen, soren f
title of invention: improved phytases

to: us-09-684-855-160  check: 1807  from: 1  to: 440

FROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/fetches/US09684855.pep
sequence 160, application us/09684855
general information:
applicant: f. hoffmann-la roche ag
title of invention: continuous fermentation process
file reference: c38435/111692 . . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/blosum62.cmp
CompCheck: 1102

       Gap Weight:     3     Average Match:    2.778
    Length Weight:     0     Average Mismatch: -2.248

          Quality:  2318          Length:    440
            Ratio: 5.304            Gaps:      1
Percent Similarity: 100.000   Percent Identity: 100.000

Match display thresholds for the alignment(s):
          | = IDENTITY
          : = 2
          . = 1

us-09-488-265-27 x us-09-684-855-160 July 2, 2002 11:26 ..

   1 NSHSCDTVDGYQCPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQV 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
   1 NSHSCDTVDGYQCPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQV 50

  51 LSRHGARYPTSSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLT 100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  51 LSRHGARYPISSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLT 100

 101 PFGENQMVNSGIKFYRRYKALARNIVPFVRASGSDRVIASAEKFIEGFQS 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 101 PFGENQMVNSGIKFYRRYKALARNIVPFVRASGSDRVIASAEKFIEGFQS 150

 151 AKLADPAHQASPVINVIIPEGSGYNNTLDHGLCTAFEDSTI...LGDDAEA 197
     ||||||||||||||||||||||||||||||||||||||      ||||||
 151 AKLADPAHQASPVINVIIPEGSGYNNTLDHGLCTAFEDSTSEQLGDDAEA 200

 198 NFTAVFAPPIRARLEALPGVNLTDEDVNLMDMCPFDTVARTSDATQLSP 247
     ||||||||||||||||||||||||||||||||||||||||||||||||
 201 NFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSP 250

 248 FCDLFTADEWQYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARLTHSPVQ 297
     |||||||||||||||||||||||||||||||||||||||||||||||||
 251 FCDLFTADEWQYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARLTHSPVQ 300

 298 DHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLST 347
     |||||||||||||||||||||||||||||||||||||||||||||||||
 301 DHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLST 350

 348 TSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVN 397
     |||||||||||||||||||||||||||||||||||||||||||||||||
 351 TSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGEGEKEPLVRVLVN 400

 398 DRVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 437
     |||||||||||||||||||||||||||||||||||||||
 401 DRVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 440
```

GAP of: us-09-488-265-26   check: 9654   from: 1   to: 467

FROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/US0948265.pep
sequence 26, application us/09488265
general information:
applicant: lehmann, martin
applicant: lassen, soren f
title of invention: improved phytases . . .

to: us-09-273-871a-9   check: 3   from: 1   to: 467

FROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/fetches/US0927871A.pep
sequence 9, application us/0927871a
general information:
applicant: svendsen, allan
title of invention: phytase variants
file reference: 5618.500-us . . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/blosum62.cmp
CompCheck: 1102

Gap Weight:	3	Average Match:	2.778
Length Weight:	0	Average Mismatch:	-2.248

Quality:	2311	Length:	467
Ratio:	4.949	Gaps:	0
Percent Similarity:	94.647	Percent Identity:	93.148

Match display thresholds for the alignment(s):
```
                    | = IDENTITY
                    : = 2
                    . = 1
```

us-09-488-265-26 x us-09-273-871a-9 July 2, 2002 10:56

```
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQ 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQ 50

 51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKKKYSALIE 100
    ||||:|||| |||||||||||||||||||||||||||||||||||||||
 51 YSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSALIE 100

101 AIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRYKAL 150
    ||||:||:||||:|||||||||||||||||||||:|||||||||||||:|
101 AIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRYKAL 150

151 ARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVI 200
    ||||:|||||:|||||||:|||||||||:||||||::|||||:|||:|||
151 ARKIVPFIRASGSDRVIASAAEKFIEGFQSAKLADPGSQPHQASPVIDVI 200

201 PEGAGYNNTILDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGV 250
    |||||||||:|||||||||||||:|||||||||:|||:||||||||||:|
201 PEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGV 250

251 NLTDEDVVNLMDMCPFDTVARTSDAIQLSPFCDLLFTHDEWIQYDLQSLG 300
    |||||||| ||||||||||||||:||||||:|||||||||:||||||:||
251 TLTDEDVVILMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLG 300

301 KYYGYGAGNPLGPAQGVGVFVNELIARLTHSPVQDHTSTNHFLDSNPATFP 350
    |||||||||||||||||||||||||||||||:||||||||||||||||||
301 KYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNHFLDSNPATFP 350

351 LNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWT 400
    |||:|||||||||:|||||||||:||||||:||||||||||||||||||
351 LNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHCCGVDKLIGRCKRDDFV 450
    ||||||||||||||||||||||||||||||:|||||||||||||||||||
401 VPFGARAYVEMMQCQOAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFV 450

451 EGLSFARSGGNWAECFA 467
    |||||||||||||| |||
451 EGLSFARSGGNWAECFA 467
```

```
GAP of: us-09-488-265-26  check: 9654  from: 1  to: 467
FROMIG of: /staff_overflow/sdavid-tmp/ju102/ramirez265/US09488265.pep
sequence 26, application us/09488265
general information:
applicant: lehmann, martin
applicant: lassen, soren f
title of invention: improved phytases . . .

to: us-09-343-126b-167  check: 7552  from: 1  to: 441
FROMIG of: /staff_overflow/sdavid-tmp/ju102/ramirez265/fetches/US09343126B.pep
sequence 167, application us/09343126b
general information:
applicant: brugger, roland
applicant: lehmann, martin
applicant: wyss, markus . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/blosum62.cmp
CompCheck: 1102

     Gap Weight:    3    Average Match:    2.778
  Length Weight:    0    Average Mismatch: -2.248

      Quality:  2344        Length:       467
        Ratio:  5.315         Gaps:         0
Percent Similarity: 100.000  Percent Identity: 100.000

Match display thresholds for the alignment(s):
         | = IDENTITY
         : = 2
         . = 1

us-09-488-265-26 x us-09-343-126b-167 July 2, 2002 10:57 ..


    1 MGVFVVLLSIATLFGSTSGTTALGPRGNSHSCDTVDGGYQCFPEISHLWGQ 50
                       |||||||||||||||||||||||
    1 .................NSHSCDTVDGGYQCFPEISHLWGQ 24

   51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKKYSALIE 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
   25 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKKYSALIE 74

  101 AIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRYKAL 150
      |||||||||||||||||||||||||||||||||||||||||||||||||
   75 AIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRYKAL 124

  151 ARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVII 200
      |||||||||||||||||||||||||||||||||||||||||||||||||
  125 ARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVII 174

  201 PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGV 250
      |||||||||||||||||||||||||||||||||||||||||||||||||
  175 PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGV 224

  251 NLTDEDVVNLMDMCPFDIVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
      |||||||||||||||||||||||||||||||||||||||||||||||||
  225 NLTDEDVVNLMDMCPFDIVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 274

  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFP 350
      |||||||||||||||||||||||||||||||||||||||||||||||||
  275 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFP 324

  351 LNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWI 400
      |||||||||||||||||||||||||||||||||||||||||||||||||
  325 LNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWI 374

  401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFV 450
      |||||||||||||||||||||||||||||||||||||||||||||||||
  375 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFV 424

  451 EGLSFARSGGNWEECFA 467
      |||||||||||||||||
  425 EGLSFARSGGNWEECFA 441
```

GAP of: us-09-488-265-26 check: 9654 from: 1 to: 467

FROMIG of: /staff_overflow/sdavid-tmp/ju102/ramirez265/US09488265.pep
sequence 26, application us/09488265
general information:
applicant: lehmann, martin
applicant: lassen, soren f
title of invention: improved phytases . . .

to: us-09-684-855-163 check: 9494 from: 1 to: 467

FROMIG of: /staff_overflow/sdavid-tmp/ju102/ramirez265/fetches/US09684855.pep
sequence 163, application us/09684855
general information:
applicant: f. hoffmann-la roche ag
title of invention: continuous fermentation process
file reference: c38435/111692 . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/blosum62.cmp
CompCheck: 1102

	Average Match: 2.778
Gap Weight: 3	Average Mismatch: -2.248
Length Weight: 0	

Quality: 2448	Length: 467
Ratio: 5.242	Gaps: 0
Percent Similarity: 99.143	Percent Identity: 98.929

Match display thresholds for the alignment(s):

```
             | = IDENTITY
             : = 2
             . = 1
```

us-09-488-265-26 x us-09-684-855-163 July 2, 2002 10:53 . .

```
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQ 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGT 50

 51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKKYSALIE 100
    ||||||||||||||||| |||||||||||||||||||| |||  ||
 51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIE 100

101 AIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRYRYKAL 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 AIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRYRYKAL 150

151 ARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVII 200
    ||:||||||||||||||||||||||||||||||||||||||||||||||
151 ARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVII 200

201 PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGV 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGV 250

251 NLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 NLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300

301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFP 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFP 350

351 LNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESTEETDGYAASWT 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 LNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESTEETDGYSASWT 400

401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFV 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFV 450

451 EGLSFARSGGNWEECFA 467
    |||||||||||||||||
451 EGLSFARSGGNWEECFA 467
```

GAP of: us-09-488-265-25   check: 291   from: 1   to: 1426

PROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/US09488265.seq
sequence 25, application us/09488265
general information:
applicant: lehmann, martin
applicant: lassen, soren f
title of invention: improved phytases . . .

to: us-09-684-855-164   check: 4581   from: 1   to: 1404

PROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/fetches/US09684855.seq
sequence 164, application us/09684855
general information:
applicant: f. hoffmann-la roche ag
title of invention: continuous fermentation process
file reference: c38435/111692 . . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000

Quality:	13940	Length:	1426
Ratio:	9.929	Gaps:	0
Percent Similarity:	99.288	Percent Identity:	99.288

Match display thresholds for the alignment(s):

```
                  |  =  IDENTITY
                  :  =  5
                  .  =  1
```

us-09-488-265-25 x us-09-684-855-164 July 2, 2002 10:50 . .

```
  1 tatatgaattcatggggcgtgttcgttcgttcgttcattgccacttg    50
    |||||||||||||||||||||||||||||||||||||||||||| .
  1 .........atgggcgtgttcgttcgtgctactgtccattgccaccttg    39

 51 ttcggttccacatccggtaccgccgcttgggctcctgcgtggtaattctcaactc   100
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 40 ttcggttccacatccggtaccgccgcttgggctcctgcgtggtaactctcaactc    89

101 ttgtgacactgttgacgtgttgttaccaaatgtttcccagaaatttctcact   150
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
 90 ttgtgacactgttgacgtgttggttaccaaatgttccagaaatttctcact   139

151 tgtggggtccaaatactctccaattctccaattctggctgacggaatctgctatt   200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
140 tgtggggtacatatctccaattctccaattctccttgctgacggaatctgctatt   189

201 tctccagacgttccaaaaggagttgtttagagttcacttcgttcaagtttgtc   250
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
190 tctccagacgttccaaaaggagttgttttagagttacttcgttcaagtttgtc   239

251 tagacacgtgttctagatacccaacttcttcttctaagtctagaagtactctg   300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
240 tagacacgtgttctagatacccaacttcttcttctagtggccgtactctg   289

301 ctttgattgaagctattcaaaagaaacgctactgcttcaaggtaagtac   350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
290 ctttgattgaagctattcaaaagaaacgctactgcttcaaggtaagtac   339

351 gctttcttgaagacttacaactacaacttgggtgctgacgactttgactcc   400
    |||||||||||||||||||||||||||||||||||||||||||||||||||
340 gctttcttgaagacttacaactacaacttgggtgctgacgactttgactcc   389

401 attccggttgaacaacaaatggttaactcttcggtattcaagttctacagaagat   450
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
390 attccggttgaacaacaaatggttaactcttcggtattcaagttctacagaagat   439

451 acaaggcttttggctagaagaagattgttccattcgttagaagcttcggttct   500
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
440 acaaggcttttggctagaagaagattgttccattcgttagaagcttcggttct   489

501 gacagagttattgcttcctgctgaaaagttcattgaaggtttccaatctgc   550
    |||||||||||||||||||||||||||||||||||||||||||||||||||
490 gacagagttattgcttcctgctgaaaagttcattgaaggtttccaatctgc   539

551 ttgtgtactgcttcgaagaatctgaattgggtgtcaacaccacacaagctgtta   600
    |||||||||||||||||||||||||||||||||||||||||||||||||||||
540 taagttggctgacccaggtgctaaccacacaagcttcctccagttatta   589

601 acgttattattcccagaaggtgctgttacaacaacacttggaccacggt   650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
590 acgttattattcccagaaggtgctgttacaacacacttggaccacggt   639

651 ttgtccattcgaacactgttgctactagaactctgacgctactcaattgtctcc   700
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
640 ttgtgtactgcttcgaagaatctgaattgggtgtcaacaccacacaagctaa   689

701 cttcactgtgttccgctccaactattagaagctgacgattggaagctaact   750
    |||||||||||||||||||||||||||||||||||||||||||||||||||
690 cttcactgctgttccgctccaccaattagagctagaatattggaagctcact   739

751 tgccaggttgttaacttgactacgaagaagacgttgttgttaacttgatggacatg   800
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
740 tgccaggttgttaacttgactacggtgttaacttgatggacatg   789

801 tgtccattcgacactgttgttagaacttctgacgctactcaattgtctcc   850
    |||||||||||||||||||||||||||||||||||||||||||||||||||
790 tgtccattcgacactgttgctagaacttctgacgctactcaattgtctcc   839

851 attctgtgacttgttcactcacgacgacgaatgattcaataacgactacttgc   900
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
840 attctgtgacttgttcactcacgacgaatgattcaataacgactacttgc   889

901 aatcttctgggtaagtaactacggttacggttctgttgaaccattgggtcca   950
    |||||||||||||||||||||||||||||||||||||||||||||||||||
890 aatcttctgggtaagtaactacggttacggttctgttaacccattgggtcca   939

951 gctcaaggtgttgtttcgttgttttcgttacgaacttgattgctaagacctaagcc   1000
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
940 gctcaaggtgttgttcgttgttttcgttaacgaactttgctaagacctaagcc   989

1001 tccagttcaagacaacacaactctactaaccacactttggacttaaccaag   1050
     ||||||||||||||||||||||||||||||||||||||||||||||||||
990 tccagttcaagacaacacaactctactaaccacactttggacttaaccaag   1039

1051 ctacttcccattgaacgctactttgtctgttacggttctacggttacccaac   1100
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1040 ctacttcccattgaacgctacttttgtctgttacggttcctcacgacaac   1089

1101 actatggtttctattttctcgcttgggtttgttttacaacgctactaagcc   1150
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1090 actatggtttctattttctcgcttgggtttgttttacaacgctactaagcc   1139

1151 attgtctactacttctgtgaatctattgaagaacaactgacggttactctg   1200
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1140 attgtctactacttctgtgaatctattgaagaacaactgacggttactctg   1189

1201 cttcttggactgttccaattcgctgctagaagcttacgttgaaatgatgcaa   1250
     |||||||||||||||||||||||||||||||||||||||||||||||||||||
1190 cttcttggactgttccaattcgctgctagaagcttacgttgaaatgatgcaa   1239

1251 tgtgaagtcgaaaaggaaccattggttagagtttggttaacgacacagagt   1300
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1240 tgtgaagtcgaaaaggaaccattggttagagtttggttaacgacacagagt   1289

1301 tgttccattgcacgttggttgttgacaagttgggtagatgtaagagag   1350
     |||||||||||||||||||||||||||||||||||||||||||||||||
1290 tgttccattgcacgttggttgttgacaagttgggtagatgtaagagag   1339

1351 acgacttcgttgaagtttcttcgctagaatctggtggttaactgggaa   1400
     |||||||||||||||||||||||||||||||||||||||||||||||||
1351 acgacttcgttgaagtttcttcgctagaatctggtggttaactgggaa   1400
```

GAP of: us-09-488-265-27 check: 2749 from: 1 to: 437

FROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/US09488265.pep
sequence 27, application us/09488265
general information:
applicant: lehmann, martin
applicant: lassen, soren f
title of invention: improved phytases . . .

to: us-09-343-126b-167 check: 7552 from: 1 to: 441

FROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/fetches/US09343126B.pep
sequence 167, application us/09343126b
general information:
applicant: brugger, roland
applicant: lehmann, martin
applicant: wyss, markus . . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/blosum62.cmp
CompCheck: 1102

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        Gap Weight:      3      Average Match:     2.778
     Length Weight:      0      Average Mismatch: -2.248

           Quality:   2195              Length:    448
             Ratio:  5.023                Gaps:     11
Percent Similarity: 97.907    Percent Identity: 97.674

Match display thresholds for the alignment(s):
    | = IDENTITY
    : = 2
    . = 1

us-09-488-265-27 x us-09-343-126b-167 July 2, 2002 11:24 ..


  1 NSHSCDTVD.GYQC.PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFV 48
    |||||||||:||||:|||||||||||||||||||||||||||||||||||
  1 NSHSCDTVDGGYQCPPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFV 50

 49 QVLSRHGARYPTSSKSKKYSALIERIQKNAT.FKGKYAFLKTYNYILGAD 97
    ||||||||||||||||||||||||||||||| .||||||||||||||||| 
 51 QVLSRHGARYPTSSKSKKYSALIEAIQKNATAAFKGKYAFLKTYNYILGAD 100

 98 DLTPFGENQMVNSGIKFYRYKALARNIVPFVRASGSDRVIASAEKFIEG 147
    ||||||| ||||||||||||||||:|||||||||||||||||||||||| 
101 DLTPFGEQQMVNSGIKFYRYKALARKIVPFVRASGSDRVIASAEKFIEG 150

148 FQSAKLADP.A..HQASPVINVIIPEGSGYNNTLDHGLCTAFEDSTLGDD 194
    ||||||||| .| ||:|||||||||||:|||||||||||||::||:|||| 
151 FQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDD 200

195 AEANFTAVFAPPIRARLEA.LPGVNLTDEDVVNLMDMCPFDTVARTSDAT 243
    :||||||||||||||||| ||||||||||||||||||||||||||||| 
201 VEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDAT 250

244 QLSPFCDLFTADEW.QYDYLQSL.KYYGYGAGNPLGPAQGVGF.NELIAR 290
    |||||||||:|||| ||||||||| ||||||||||||||||| :|||| 
251 QLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 300

291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYN 340
    ||||||||||||||||||||||||||||||||||||||||||||||||| 
301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYN 350

341 GTKPLSTPISVESI.ETDGYAASWTVPFAARAYVEMMQCEAGGGGEGEKE 389
    |||||||||||||| |||||||||||||||||||||||||||     ||| 
351 GTKPLSTPISVESIEETDGYAASWTVPFAARAYVEMMQCEA......EKE 393

390 PLVRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 437
    ||||||||||||||||||||||||||:|||||||||||||||||:|||| 
394 PLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 441
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